OM protein - protein search, using sw model

Run on: March 4, 2006, 07:18:16 ; Search time 38 Seconds
(without alignments)
15.192 Million cell updates/sec

Title: US-10-697-886-2
Perfect score: 31
Sequence: 1 KVLRRH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	31	100.0	134	1	AWHUB	natriuretic peptid
2	31	100.0	541	2	D97930	conserved hypothet
3	30	96.8	127	1	LZPY	lysozyme (EC 3.2.1
4	30	96.8	238	2	H81069	transcription regu
5	28	90.3	37	2	E75312	ribosomal protein
6	28	90.3	176	1	S74642	hypothetical prote
7	28	90.3	184	2	C75362	conserved hypothet
8	28	90.3	194	2	S45561	RNA polymerase sig
9	28	90.3	246	2	B48350	infected-cell prot
10	28	90.3	277	2	A83721	nickel transport s
11	28	90.3	319	2	AF0228	probable transposa
12	28	90.3	340	2	T35394	probable glycerol
13	28	90.3	388	2	T36402	probable monooxyge
14	28	90.3	417	2	F95953	probable glycosylt
15	28	90.3	444	2	AH3174	glutamate-1-semial
16	28	90.3	459	2	H84030	glutamyl-tRNA redu
17	28	90.3	505	2	C84731	probable beta-amyl
18	28	90.3	604	2	B90289	conserved hypothet
19	28	90.3	824	2	AB2829	DNA helicase II [i
20	28	90.3	827	2	H97606	probable DNA helic
21	28	90.3	827	2	AF3326	DNA helicase II (E
22	27	87.1	136	2	F81451	peroxide stress re
23	27	87.1	152	2	C72681	hypothetical prote
24	27	87.1	183	1	D64430	probable transcrip
25	27	87.1	196	2	S06581	finger protein (cl
26	27	87.1	197	2	T35766	hypothetical prote
27	27	87.1	211	2	E75305	hypothetical prote
28	27	87.1	250	2	A61153	spectinomycin aden
29	27	87.1	252	2	B81053	beta-1,4-glucosylt
30	27	87.1	254	2	D81824	beta-1,4-glucosylt
31	27	87.1	263	1	H64069	beta-lactamase reg
32	27	87.1	334	2	B83488	probable L-malate
33	27	87.1	350	2	T03291	farnesyl-pyrophosp
34	27	87.1	360	2	T26037	hypothetical prote
35	27	87.1	360	2	S32695	Wnt-2 protein - Ca
36	27	87.1	380	2	S17676	NADH2 dehydrogenas
37	27	87.1	406	2	E72366	conserved hypothet
38	27	87.1	443	2	C71904	anaerobic c4-dicar
39	27	87.1	443	2	D64610	dicarboxylate memb
40	27	87.1	469	2	A71369	probable sugar ABC
41	27	87.1	487	1	QQBEU5	UL37 protein precu
42	27	87.1	570	2	G85046	hypothetical prote
43	27	87.1	571	2	AG3174	acetolactate synth
44	27	87.1	642	2	T41690	conserved hypothet
45	27	87.1	678	2	C72319	flagellar biosynth

ALIGNMENTS

RESULT 1
AWHUB
natriuretic peptide B precursor [validated] - human
N;Alternate names: brain natriuretic factor-32 (BNF-32); brain natriuretic protein prec
N;Contains: brain alpha natriuretic peptide; brain gamma natriuretic factor
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: A36736; A30163; A34143; A34661; B34661
R;Seilhamer, J.J.; Arfsten, A.; Miller, J.A.; Lundquist, P.; Scarborough, R.M.; Lewicki
Biochem. Biophys. Res. Commun. 165, 650-658, 1989
A;Title: Human and canine gene homologs of porcine brain natriuretic peptide.
A;Reference number: A36736; MUID:90088474; PMID:2597152
A;Accession: A36736
A;Molecule type: DNA
A;Residues: 1-134 <SEI>
A;Cross-references: UNIPROT:P16860; UNIPARC:UPI00000350A5; GB:M31776; NID:g179514; PIDN
R;Sudoh, T.; Maekawa, K.; Kojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 159, 1427-1434, 1989
A;Title: Cloning and sequence analysis of cDNA encoding a precursor for human brain nat
A;Reference number: A30163; MUID:89193743; PMID:2522777
A;Accession: A30163
A;Molecule type: mRNA
A;Residues: 1-134 <SUD>
A;Cross-references: UNIPARC:UPI00000350A5; GB:M31776; NID:g179514; PIDN:AAA35603.1; PID
R;Kambayashi, Y.; Nakao, K.; Mukoyama, M.; Saito, Y.; Ogawa, Y.; Shiono, S.; Inouye, K.
FEBS Lett. 259, 341-345, 1990
A;Title: Isolation and sequence determination of human brain natriuretic peptide in hum
A;Reference number: A34143; MUID:90092577; PMID:2136732
A;Accession: A34143
A;Molecule type: protein
A;Residues: 103-134 <KAM>
A;Cross-references: UNIPARC:UPI00000350A8
R;Hino, J.; Tateyama, H.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 167, 693-700, 1990
A;Title: Isolation and identification of human brain natriuretic peptides in cardiac at
A;Reference number: A90161; MUID:90211249; PMID:2138890
A;Accession: A34661
A;Molecule type: protein
A;Residues: 27-58 <HIN>
A;Cross-references: UNIPARC:UPI00001733AB
A;Accession: B34661
A;Molecule type: protein
A;Residues: 103-134 <HI2>
A;Cross-references: UNIPARC:UPI00001733AB
C;Genetics:
A;Gene: GDB:NPPB
A;Cross-references: GDB:127884; OMIM:600295
A;Map position: 1p36-1p36
A;Introns: 44/3; 130/1
C;Superfamily: natriuretic peptide A precursor
C;Keywords: brain; diuretic; hormone; natriuretic; osmoregulation
F;1-26/Domain: signal sequence #status predicted <SIG>

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 4, 2006; 07:14:47 ; Search time 185 Seconds
(without alignments)
14.250 Million cell updates/sec

Title: US-10-697-886-2
Perfect score: 31
Sequence: 1 KVLRRH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	31	100.0	6	2	AAW51290	Aaw51290 Human B-t
2	31	100.0	6	3	AAY80220	Aay80220 Human B-t
3	31	100.0	6	8	ADP49271	Adp49271 Natriuret
4	31	100.0	15	8	ADJ79686	Adj79686 Human Bra
5	31	100.0	21	2	AAW25774	Aaw25774 Human bra
6	31	100.0	23	8	ADL22365	Adl22365 Natriuret
7	31	100.0	23	8	ADL22362	Adl22362 Natriuret
8	31	100.0	23	8	ADL22364	Adl22364 Natriuret
9	31	100.0	23	8	ADL22361	Adl22361 Natriuret
10	31	100.0	23	8	ADL22358	Adl22358 Natriuret
11	31	100.0	23	8	ADL22359	Adl22359 Natriuret
12	31	100.0	24	4	AAB46799	Aab46799 Human bra
13	31	100.0	24	8	ADL22366	Adl22366 Natriuret
14	31	100.0	24	8	ADL22360	Adl22360 Natriuret
15	31	100.0	24	8	ADL22363	Adl22363 Natriuret
16	31	100.0	25	8	ADL22352	Adl22352 Natriuret
17	31	100.0	25	8	ADL22356	Adl22356 Natriuret
18	31	100.0	25	8	ADL22355	Adl22355 Natriuret
19	31	100.0	26	3	AAY67295	Aay67295 Human bra
20	31	100.0	26	8	ADL22357	Adl22357 Natriuret
21	31	100.0	26	8	ADL22354	Adl22354 Natriuret
22	31	100.0	30	3	AAY67297	Aay67297 Human bra
23	31	100.0	31	2	AAR34302	Aar34302 Mutated B
24	31	100.0	32	2	AAR40861	Aar40861 BNP. 3/19
25	31	100.0	32	2	AAR34301	Aar34301 Mutated h
26	31	100.0	32	2	AAR36381	Aar36381 Recombina
27	31	100.0	32	2	AAW70090	Aaw70090 Brain nat
28	31	100.0	32	2	AAW67040	Aaw67040 Brain nat
29	31	100.0	32	2	AAW51263	Aaw51263 Human B-t
30	31	100.0	32	2	AAW51270	Aaw51270 Human B-t
31	31	100.0	32	2	AAW51258	Aaw51258 Human B-t
32	31	100.0	32	2	AAW51305	Aaw51305 Human B-t
33	31	100.0	32	2	AAW51259	Aaw51259 B-type na
34	31	100.0	32	2	AAW51260	Aaw51260 Type-B na
35	31	100.0	32	2	AAW51279	Aaw51279 Human B-t
36	31	100.0	32	2	AAW51300	Aaw51300 Human B-t
37	31	100.0	32	2	AAW51273	Aaw51273 Human B-t
38	31	100.0	32	2	AAW51274	Aaw51274 Human B-t
39	31	100.0	32	2	AAW51265	Aaw51265 Human B-t
40	31	100.0	32	2	AAW51269	Aaw51269 Human B-t
41	31	100.0	32	2	AAW51277	Aaw51277 Human B-t
42	31	100.0	32	2	AAW51283	Aaw51283 Human B-t
43	31	100.0	32	2	AAW51276	Aaw51276 Human B-t
44	31	100.0	32	2	AAW51286	Aaw51286 Human B-t
45	31	100.0	32	2	AAW51266	Aaw51266 Human B-t

ALIGNMENTS

RESULT 1
AAW51290
ID AAW51290 standard; peptide; 6 AA.
XX
AC AAW51290;
XX
DT 15-SEP-1998 (first entry)
XX
DE Human B-type natriuretic peptide variant partial sequence.
XX
KW B-type natriuretic peptide; clearance receptor; electrolyte balance;
KW diuretic; vasodilator; circulation; natriuresis; diuresis; hNPR-C;
KW cyclic guanosine monophosphate; cGMP; second messenger; variant.
XX
OS Synthetic.
XX
PN WO9817690-A1.
XX
PD 30-APR-1998.
XX
PF 09-OCT-1997; 97WO-US018384.
XX
PR 22-OCT-1996; 96US-00731880.
XX
PA (GETH) GENENTECH INC.
XX
PI Lowe DG, Schoenfeld JR;
XX
DR WPI; 1998-261429/23.
XX
PT Variants of brain natriuretic peptide with reduced affinity for clearance
PT receptor - for treating disorders of electrolyte balance and as diuretics
PT and vasodilators, have increased circulation time and in vivo activity.
XX
PS Claim 7; Page 46; 55pp; English.
XX
CC The invention relates to variants of brain natriuretic peptide (BNP) with
CC reduced affinity for the human clearance receptor (hNPR-C) relative to
CC wild-type BNP. The variants are used: (a) to treat or prevent disorders
CC of electrolyte balance, or (b) to induce natriuresis, diuresis or
CC vasodilation. Typical applications are in congestive heart failure,
CC arrhythmia, hypertension, nephrotic syndrome, pre-eclampsia, premenstrual
CC syndrome, hepatic cirrhosis, pulmonary disease and renal failure
CC (associated with inefficient renal perfusion or reduced glomerular
CC filtration rate). The variants are also useful as intermediates and as
CC modulators of other compounds with similar activities. Although the
CC variants have reduced affinity for NPR-C, they have at least equal